

## RAW SEQUENCE LISTING

DATE: 05/14/2001

PATENT APPLICATION: US/09/670,106

TIME: 11:35:06

Input Set : N:\Crif3\RULE60\09670106.txt

Output Set: N:\CRF3\05142001\I670106.raw

## SEQUENCE LISTING

ENTERED

4 (1) GENERAL INFORMATION:  
6 (i) APPLICANT: BLACK, ROY A  
7 SLEATH, PAUL R  
8 KRONHEIM, SHIRLEY R  
10 (ii) TITLE OF INVENTION: INTERLEUKIN 1B PROTEASE AND  
11 INTERLEUKIN 1B PROTEASE INHIBITORS  
14 (iii) NUMBER OF SEQUENCES: 24  
16 (iv) CORRESPONDENCE ADDRESS:  
17 (A) ADDRESSEE: DRESSLER, GOLDSMITH, SHORE, SUTKER &  
18 MILNAMOW  
20 (B) STREET: 180 N. STETSON  
21 (C) CITY: CHICAGO  
22 (D) STATE: IL  
23 (E) COUNTRY: USA  
24 (F) ZIP: 60601  
26 (v) COMPUTER READABLE FORM:  
27 (A) MEDIUM TYPE: Floppy disk  
28 (B) COMPUTER: IBM PC compatible  
29 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
30 (D) SOFTWARE: PatentIn Release #1.24  
32 (vi) CURRENT APPLICATION DATA:  
C--> 33 (A) APPLICATION NUMBER: US/09/670,106  
C--> 34 (B) FILING DATE: 26-Sep-2000  
36 (vii) PRIOR APPLICATION DATA:  
37 (A) APPLICATION NUMBER: US/08/203,716  
38 (B) FILING DATE: 08-FEB-1994  
39 (A) APPLICATION NUMBER: US/07/750,644  
40 (B) FILING DATE:  
42 (viii) ATTORNEY/AGENT INFORMATION:  
43 (A) NAME: KATZ, MARTIN L.  
44 (B) REGISTRATION NUMBER: 25011  
45 (C) REFERENCE/DOCKET NUMBER: IMMUNEX2108  
47 (ix) TELECOMMUNICATION INFORMATION:  
48 (A) TELEPHONE: 3126165400  
49 (B) TELEFAX: 3126165460  
50 (C) TELEX: 9102211206  
53 (2) INFORMATION FOR SEQ ID NO: 1:  
55 (i) SEQUENCE CHARACTERISTICS:  
56 (A) LENGTH: 1659 base pairs  
57 (B) TYPE: nucleic acid  
58 (C) STRANDEDNESS: single  
59 (D) TOPOLOGY: linear  
60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
62 AAAAGGAGAG AAAAGCCTAA AAGAGAGTGG GTAGATGGCC GACAAGGTCC TGAAGGAGAA 60  
64 GAGAAAGCTG TTTATCCGTT CCATGGGTGA AGGTACAATA AATGGCTTAA GGTAGAAGGT 120  
66 GAAGGAAATA CTGGATGAAT TATTACAGAC AAGGGTGCTG AACAAGGAAG AGATGGAGAA 180

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68 AGTAAAACGT GAAAATGCTA CAGTTTATAG AAAAGAAGAA CGCTTATGGA TAAGACCCGA 240
70 GCTTTGATTG ACTCCGTTAT TCCGAAAGGG GCACAGGCAT GCCAAATTTG CATCACATAC 300
72 CGGATAAGTG AAAGTGATAA TTTGTGAAGA AGACAGTTAC CTGGCAGGGA CGCTGGGACT 360
74 CTCAGCAGAT CAAACATCTG GAAATTACCT TAATTGAGGA AAGAAAGAAA ATTATGCAAG 420
76 ACTCTCAAGG AGTACTTTCT TCCTTTCCAG CTCCTCAGGC AGTGCAGGAC AACCCAGCTA 480
78 TGCCACAGG GAACGGAAGA GTGAATCCTC AGGCTCAGAA GGAATGTCA AGCTTTGCTC 540
80 CCTAGAAGAA GCTCAAAGGA TATGGAAACA AAAGTCGGCA GTTAAGTAGA ACAGGAGAGA 600
82 TTTATCCAAT AATGGACAAG TCAAGCCGCA CACGTCTTGC TCTCATTATC TGCAATGAAG 660
84 AATTTGACAG TAGAGTGAAG AATGTTTGAG TAATTCCTAG AAGAACTGGA GCTGAGGTTG 720
86 ACATCACAGG CATGACAATG CTGCTACAAA ATCTGGGGTA CAGCGTAAAA TAAATTTGGA 780
88 AAAAGGGATG TGAAAAAAA TCTCACTGCT TCGGACATGA CTACAGAGCT GGAGGCATTT 840
90 GCACACCGCC CAGAGCACAA GTATATGAGG GCGGACCTCT GACAGCACGT TCCTGGTGTT 900
92 CATGTCTCAT GGTATTCGGG AAGGCATTTG TGGGAAGAAA CACTCTGAGG AAGAAAATAT 960
94 ACACAAGTCC CAGATATACT ACAACTCAAT GCAATCTTTA ACATGTTGAA TACCAAGAAC 1020
96 TGCCCAAGTT TGAAGGACAG AACAGGAGAA TAAGAAACCG AAGGTGATCA TCATCCAGGC 1080
98 CTGCCGTGGT GACAGCCCTG GTGTGGTGTG GTTTAAAGAT TCAGTAGGAA GATTGGGAAA 1140
100 AAAGGTTTCT GGAAACCTAT CTTTACCAAC TACAGAAGAG TTTGAGGATG ATGCTATTAA 1200
102 GAAAGCCCAC ATAGAGAAGA AACTAAATAG TTGAGATTTT ATCGCTTTCT GCTCTTCCAC 1260
104 ACCAGATAAT GTTCTTGGA GACATCCCAC AATGGGCTCT GTTTTATTG AGGTGGTAAC 1320
106 CAAGGAGAAG GGAAGACTCA TTGAACATAT GCAAGAATAT GCCTGTTTCT GTGATGTGGA 1380
108 GGAAATTTTC CGCAAGGTTT GATTGGGAGA GAAGTTTGAG ATTAGCTTCA TTTGAGCAGC 1440
110 CAGATGGTAG AGCGCAGATG CCCACCACTG AAAGAGTGAC TTTGACAAGA TGTTTCTACC 1500
112 TCGTTCCCAG GACATTAAAA TAAGGAAACT GTATGAATGT CTGCGGGCAG GAAGTGAAGA 1560
114 GATCGTTCTG TAAAGGTTT TTGAATTAT GTCTGCTGAA TAATAAACTT TTTTGAAT 1620
116 AATAAATCTG GTAGAAAAAT GAAAAAATAA AAAAAAATAA 1659

```

121 (2) INFORMATION FOR SEQ ID NO: 2:

123 (i) SEQUENCE CHARACTERISTICS:

124 (A) LENGTH: 404 amino acids

125 (B) TYPE: amino acid

126 (D) TOPOLOGY: linear

127 (ii) MOLECULE TYPE: peptide

129 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```

131 Met Ala Asp Lys Val Leu Lys Glu Lys Arg Lys Leu Phe Ile Arg Ser
132 1 5 10 15
134 Met Gly Glu Gly Thr Ile Asn Gly Leu Leu Asp Glu Leu Leu Gln Thr
135 20 25 30
137 Arg Val Leu Asn Lys Glu Glu Met Glu Lys Val Lys Arg Glu Asn Ala
138 35 40 45
140 Thr Val Met Asp Lys Thr Arg Ala Leu Ile Asp Ser Val Ile Pro Lys
141 50 55 60
143 Gly Ala Gln Ala Cys Gln Ile Cys Ile Thr Tyr Ile Cys Glu Glu Asp
144 65 70 75 80
146 Ser Tyr Leu Ala Gly Thr Leu Gly Leu Ser Ala Asp Gln Thr Ser Gly
147 85 90 95
149 Asn Tyr Leu Asn Met Gln Asp Ser Gln Gly Val Leu Ser Ser Phe Pro
150 100 105 110
152 Ala Pro Gln Ala Val Gln Asp Asn Pro Ala Met Pro Thr Ser Ser Gly
153 115 120 125
155 Ser Glu Gly Asn Val Lys Leu Cys Ser Leu Glu Glu Ala Gln Arg Ile

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```

156      130      135      140
158 Trp Lys Gln Lys Ser Ala Glu Ile Tyr Pro Ile Met Asp Lys Ser Ser
159 145      150      155      160
161 Arg Thr Arg Leu Ala Leu Ile Ile Cys Asn Glu Glu Phe Asp Ser Ile
162      165      170      175
164 Pro Arg Arg Thr Gly Ala Glu Val Asp Ile Thr Gly Met Thr Met Leu
165      180      185      190
167 Leu Gln Asn Leu Gly Tyr Ser Val Asp Val Lys Lys Asn Leu Thr Ala
168      195      200      205
170 Ser Asp Met Thr Thr Glu Leu Glu Ala Phe Ala His Arg Pro Glu His
171      210      215      220
173 Lys Thr Ser Asp Ser Thr Phe Leu Val Phe Met Ser His Gly Ile Arg
174 225      230      235      240
176 Glu Gly Ile Cys Gly Lys Lys His Ser Glu Gln Val Pro Asp Ile Leu
177      245      250      255
179 Gln Leu Asn Ala Ile Phe Asn Met Leu Asn Thr Lys Asn Cys Pro Ser
180      260      265      270
182 Leu Lys Asp Lys Pro Lys Val Ile Ile Gln Ala Cys Arg Gly Asp
183      275      280      285
185 Ser Pro Gly Val Val Trp Phe Lys Asp Ser Val Gly Val Ser Gly Asn
186      290      295      300
188 Leu Ser Leu Pro Thr Thr Glu Glu Phe Glu Asp Asp Ala Ile Lys Lys
189 305      310      315      320
191 Ala His Ile Glu Lys Asp Phe Ile Ala Phe Cys Ser Ser Thr Pro Asp
192      325      330      335
194 Asn Val Ser Trp Arg His Pro Thr Met Gly Ser Val Phe Ile Gly Arg
195      340      345      350
197 Leu Ile Glu His Met Gln Glu Tyr Ala Cys Ser Cys Asp Val Glu Glu
198      355      360      365
200 Ile Phe Arg Lys Val Arg Phe Ser Phe Glu Gln Pro Asp Gly Arg Ala
201      370      375      380
203 Gln Met Pro Thr Thr Glu Arg Val Thr Leu Thr Arg Cys Phe Tyr Leu
204 385      390      395      400
206 Phe Pro Gly His

```

211 (2) INFORMATION FOR SEQ ID NO: 3:

213 (i) SEQUENCE CHARACTERISTICS:

214 (A) LENGTH: 269 amino acids

215 (B) TYPE: amino acid

216 (D) TOPOLOGY: linear

217 (ii) MOLECULE TYPE: peptide

219 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

```

221 Met Ala Glu Val Pro Glu Leu Ala Ser Glu Met Met Ala Tyr Tyr Ser
222 1      5      10      15
224 Gly Asn Glu Asp Asp Leu Phe Phe Glu Ala Asp Gly Pro Lys Gln Met
225      20      25      30
227 Lys Cys Ser Phe Gln Asp Leu Asp Leu Cys Pro Leu Asp Gly Gly Ile
228      35      40      45
230 Gln Leu Arg Ile Ser Asp His His Tyr Ser Lys Gly Phe Arg Gln Ala
231      50      55      60

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```

233 Ala Ser Val Val Val Ala Met Asp Lys Leu Arg Lys Met Leu Val Pro
234 65                               70                               75                               80
236 Cys Pro Gln Thr Phe Gln Glu Asn Asp Leu Ser Thr Phe Phe Pro Phe
237                               85                               90                               95
239 Ile Phe Glu Glu Glu Pro Ile Phe Phe Asp Thr Trp Asp Asn Glu Ala
240                               100                              105                              110
242 Tyr Val His Asp Ala Pro Val Arg Ser Leu Asn Cys Thr Leu Arg Asp
243                               115                              120                              125
245 Ser Gln Gln Lys Ser Leu Val Met Ser Gly Pro Tyr Glu Leu Lys Ala
246                               130                              135                              140
248 Leu His Leu Gln Gly Gln Asp Met Glu Gln Gln Val Val Phe Ser Met
249 145                               150                              155                              160
251 Ser Phe Val Gln Gly Glu Glu Ser Asn Asp Lys Ile Pro Val Ala Leu
252                               165                              170                              175
254 Gly Leu Lys Glu Lys Asn Leu Tyr Leu Ser Cys Val Leu Lys Asp Asp
255                               180                              185                              190
257 Lys Pro Thr Leu Gln Leu Glu Ser Val Asp Pro Lys Asn Tyr Pro Lys
258                               195                              200                              205
260 Lys Lys Met Glu Lys Arg Phe Val Phe Asn Lys Ile Glu Ile Asn Asn
261                               210                              215                              220
263 Lys Leu Glu Phe Glu Ser Ala Gln Phe Pro Asn Trp Tyr Ile Ser Thr
264 225                               230                              235                              240
266 Ser Gln Ala Glu Asn Met Pro Val Phe Leu Gly Gly Thr Lys Gly Gly
267                               245                              250                              255
268 Gln Asp Ile Thr Asp Phe Thr Met Gln Phe Val Ser Ser
269                               260                              265

```

274 (2) INFORMATION FOR SEQ ID NO: 4:

276 (i) SEQUENCE CHARACTERISTICS:

277 (A) LENGTH: 18 base pairs

278 (B) TYPE: nucleic acid

279 (C) STRANDEDNESS: single

280 (D) TOPOLOGY: linear

W--&gt; 281 (ii) MOLECULE TYPE: DNA

283 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

285 TACCGGCTGT TCCAGGAC 18

290 (2) INFORMATION FOR SEQ ID NO: 5:

292 (i) SEQUENCE CHARACTERISTICS:

293 (A) LENGTH: 18 base pairs

294 (B) TYPE: nucleic acid

295 (C) STRANDEDNESS: single

296 (D) TOPOLOGY: linear

W--&gt; 297 (ii) MOLECULE TYPE: DNA

299 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

301 TACCTATTCT GGGCTCGA 18

306 (2) INFORMATION FOR SEQ ID NO: 6:

308 (i) SEQUENCE CHARACTERISTICS:

309 (A) LENGTH: 17 base pairs

310 (B) TYPE: nucleic acid

311 (C) STRANDEDNESS: single

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Output Set: N:\CRF3\05142001\I670106.raw

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312          (D) TOPOLOGY: linear
W--> 313      (ii) MOLECULE TYPE: DNA
315          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
317 TTGGTCGATA CGGGTGT 17
320 (2) INFORMATION FOR SEQ ID NO: 7:
322      (i) SEQUENCE CHARACTERISTICS:
323          (A) LENGTH: 18 base pairs
324          (B) TYPE: nucleic acid
325          (C) STRANDEDNESS: single
326          (D) TOPOLOGY: linear
W--> 327      (ii) MOLECULE TYPE: DNA
329          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
331 CACCACACCA AATTTCTA 18
336 (2) INFORMATION FOR SEQ ID NO: 8:
338      (i) SEQUENCE CHARACTERISTICS:
339          (A) LENGTH: 18 base pairs
340          (B) TYPE: nucleic acid
341          (C) STRANDEDNESS: single
342          (D) TOPOLOGY: linear
W--> 343      (ii) MOLECULE TYPE: DNA
345          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
347 ATGGAGAAGG GTCCTGTA 18
352 (2) INFORMATION FOR SEQ ID NO: 9:
354      (i) SEQUENCE CHARACTERISTICS:
355          (A) LENGTH: 26 base pairs
356          (B) TYPE: nucleic acid
357          (C) STRANDEDNESS: single
358          (D) TOPOLOGY: linear
W--> 359      (ii) MOLECULE TYPE: DNA
361          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
363 GTCGAATTCA AYCCNGCNAT GCCNAC 26
368 (2) INFORMATION FOR SEQ ID NO: 10:
370      (i) SEQUENCE CHARACTERISTICS:
371          (A) LENGTH: 26 base pairs
372          (B) TYPE: nucleic acid
373          (C) STRANDEDNESS: single
374          (D) TOPOLOGY: linear
W--> 375      (ii) MOLECULE TYPE: DNA
377          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
379 GTCTCTAGAA GYTTNACRTT NCCYTC 26
384 (2) INFORMATION FOR SEQ ID NO: 11:
386      (i) SEQUENCE CHARACTERISTICS:
387          (A) LENGTH: 43 base pairs
388          (B) TYPE: nucleic acid
389          (C) STRANDEDNESS: single
390          (D) TOPOLOGY: linear
W--> 391      (ii) MOLECULE TYPE: DNA
393          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
395 ATATCGGTAC CGCCTCCAGC ATGCCTCCGG CAATGCCCAC ATC 43

```

## VERIFICATION SUMMARY

DATE: 05/14/2001

PATENT APPLICATION: US/09/670,106

TIME: 11:35:07

Input Set : N:\CrF3\RULE60\09670106.txt

Output Set: N:\CRF3\05142001\I670106.raw

L:33 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:34 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:281 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=4  
L:297 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=5  
L:313 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=6  
L:327 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=7  
L:343 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=8  
L:359 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=9  
L:375 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=10  
L:391 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=11  
L:407 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=12  
L:476 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16